



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:25 AM GMT

PDB ID : 2QKI
Title : Human C3c in complex with the inhibitor compstatin
Authors : Janssen, B.J.C.; Halff, E.F.; Lambris, J.D.; Gros, P.
Deposited on : 2007-07-11
Resolution : 2.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

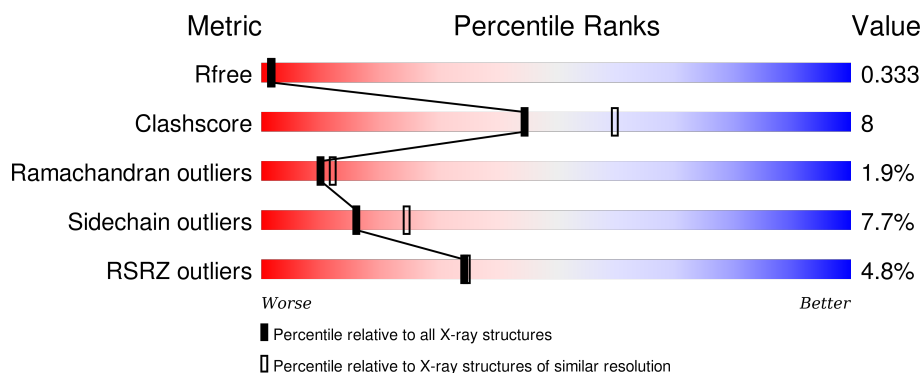
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	643	<div> <div>6%</div> <div> <div></div> <div>74%</div> <div>20%</div> <div>• •</div> </div> </div>
1	D	643	<div> <div>%</div> <div> <div></div> <div>73%</div> <div>21%</div> <div>• • •</div> </div> </div>
2	B	188	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>18%</div> <div>• •</div> </div> </div>
2	E	188	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>• •</div> </div> </div>
3	C	343	<div> <div>9%</div> <div> <div></div> <div>68%</div> <div>15%</div> <div>• 15%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	343	
4	G	15	
4	H	15	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	NAG	D	3000	X	-	-	-
6	K	D	3003	-	-	-	X
8	GOL	A	802	-	-	-	X
8	GOL	A	809	-	-	X	-
8	GOL	A	816	-	-	-	X
8	GOL	A	821	-	-	-	X
8	GOL	D	822	-	-	-	X
8	GOL	D	823	-	-	-	X
8	GOL	E	916	-	-	X	-
8	GOL	F	840	-	-	X	-
8	GOL	H	820	-	-	-	X

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 18480 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	631	Total	C	N	O	S	0	0	0
			4912	3131	831	935	15			
1	D	632	Total	C	N	O	S	0	0	0
			4919	3137	829	938	15			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	292	LEU	PRO	SEE REMARK 999	UNP P01024
D	292	LEU	PRO	SEE REMARK 999	UNP P01024

- Molecule 2 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	184	Total	C	N	O	S	0	0	0
			1484	954	250	275	5			
2	E	186	Total	C	N	O	S	0	0	0
			1500	964	252	279	5			

- Molecule 3 is a protein called Complement C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	292	Total	C	N	O	S	0	0	0
			2372	1497	388	467	20			
3	F	295	Total	C	N	O	S	0	0	0
			2395	1510	392	473	20			

- Molecule 4 is a protein called compstatin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	15	Total	C	N	O	S	0	0	1
			113	71	22	18	2			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	H	15	Total	C	N	O	S	0	0	1
			113	71	22	18	2			

- Molecule 5 is a polymer of unknown type called SUGAR (2-mer).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		
5	D	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	K	0	0
			1	1		
6	D	2	Total	K	0	0
			2	2		
6	C	1	Total	K	0	0
			1	1		
6	F	1	Total	K	0	0
			1	1		

- Molecule 7 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	15	Total	Br	0	0
			15	15		
7	E	3	Total	Br	0	0
			3	3		
7	B	3	Total	Br	0	0
			3	3		
7	C	1	Total	Br	0	0
			1	1		
7	A	8	Total	Br	0	0
			8	8		
7	F	2	Total	Br	0	0
			2	2		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			6	3	3		
8	B	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	E	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	E	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	C	1	Total	C	O	0	0
			6	3	3		
8	H	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total	C	O	0	0
			6	3	3		
8	D	1	Total	C	O	0	0
			6	3	3		
8	F	1	Total	C	O	0	0
			6	3	3		
8	A	1	Total	C	O	0	0
			6	3	3		

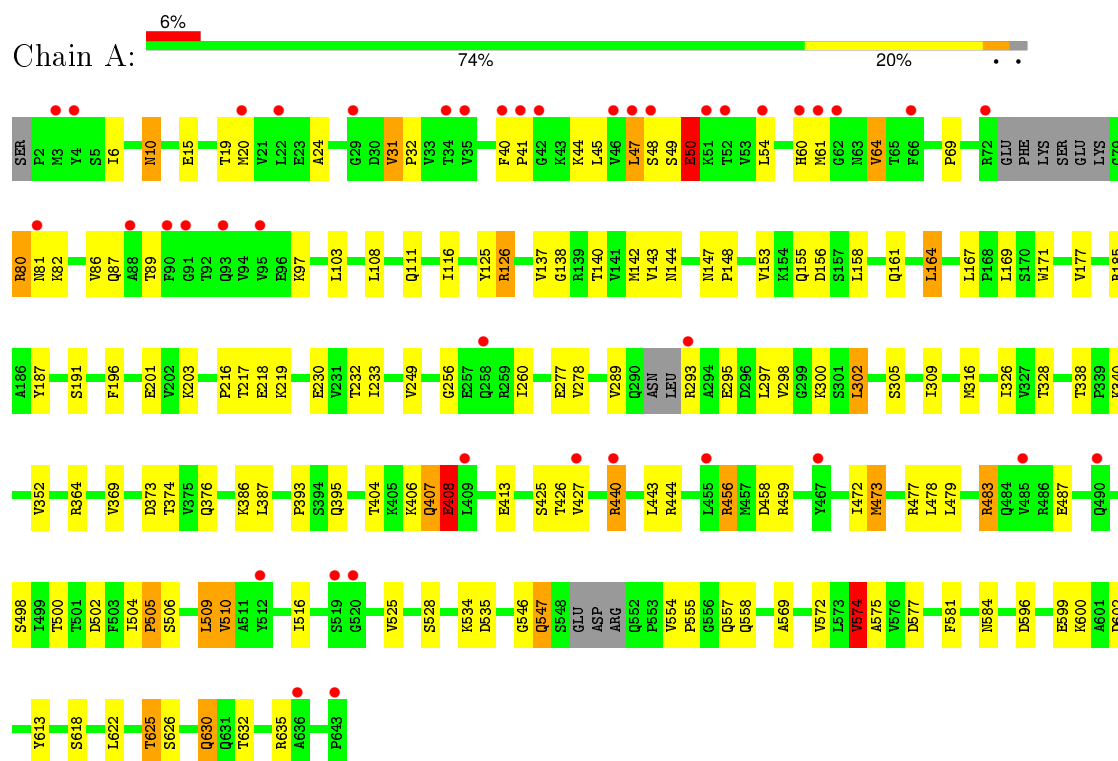
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	111	Total	O	0	0
			111	111		
9	B	47	Total	O	0	0
			47	47		
9	C	23	Total	O	0	0
			23	23		
9	D	188	Total	O	0	0
			188	188		
9	E	62	Total	O	0	0
			62	62		
9	F	35	Total	O	0	0
			35	35		
9	H	5	Total	O	0	0
			5	5		

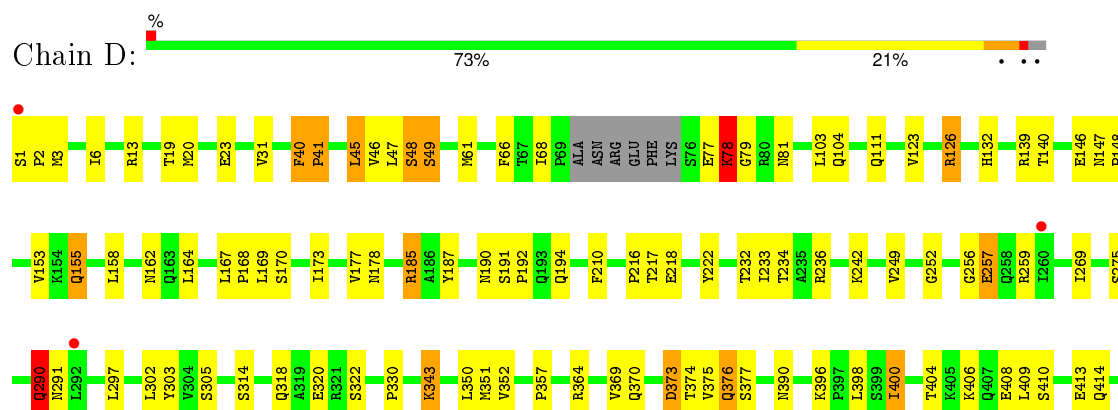
3 Residue-property plots

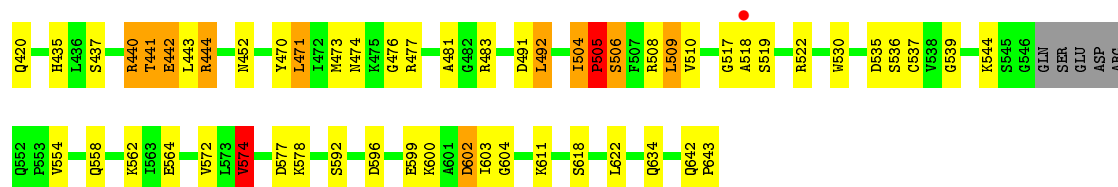
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Complement C3

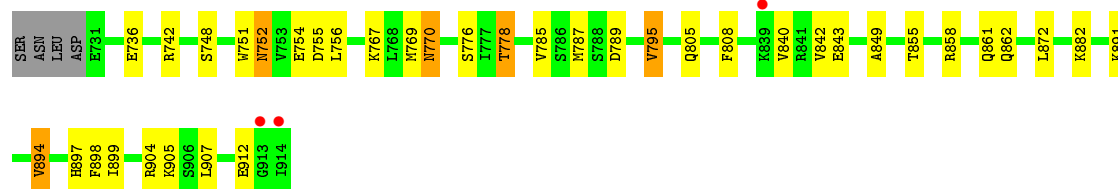
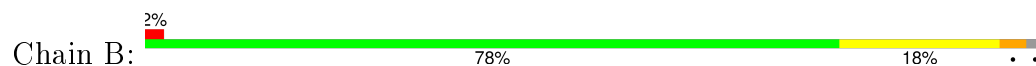


• Molecule 1: Complement C3

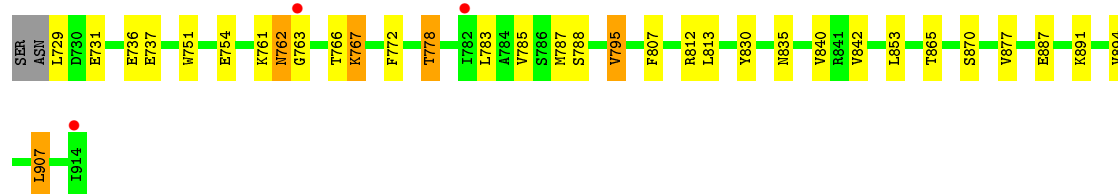
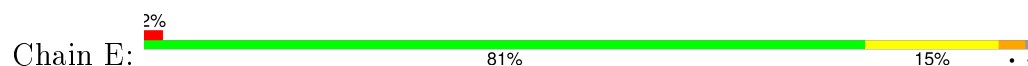




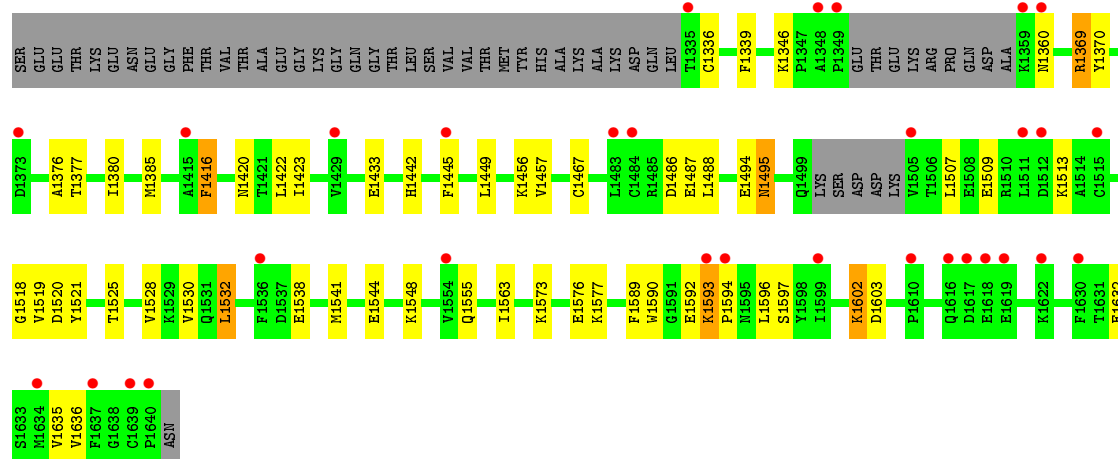
• Molecule 2: Complement C3



• Molecule 2: Complement C3

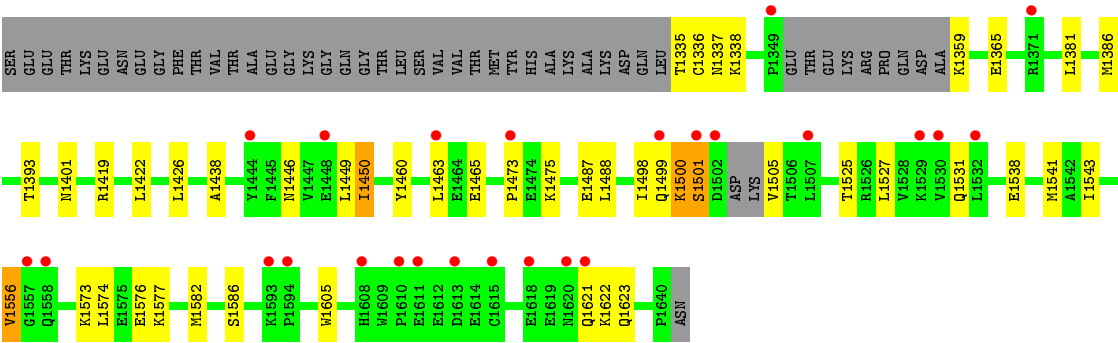


• Molecule 3: Complement C3



• Molecule 3: Complement C3

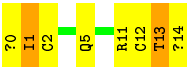




● Molecule 4: compstatin



● Molecule 4: compstatin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.81Å 124.75Å 127.37Å 90.00° 95.08° 90.00°	Depositor
Resolution (Å)	33.00 – 2.40 32.77 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.3 (33.00-2.40) 96.2 (32.77-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.3.0008	Depositor
R, R_{free}	0.213 , 0.281 0.279 , 0.333	Depositor DCC
R_{free} test set	5005 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.515	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 22.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 100445 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	18480	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, ACE, K, BR, NH2

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	1/5009 (0.0%)	0.71	3/6804 (0.0%)
1	D	0.52	0/5017	0.70	3/6817 (0.0%)
2	B	0.47	0/1516	0.63	0/2060
2	E	0.52	0/1532	0.67	0/2082
3	C	0.85	10/2418 (0.4%)	0.63	3/3261 (0.1%)
3	F	0.45	0/2441	0.57	0/3291
4	G	0.39	0/114	0.56	0/156
4	H	0.56	0/114	0.82	0/156
All	All	0.55	11/18161 (0.1%)	0.67	9/24627 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	4
3	C	0	1
5	D	1	0
All	All	1	5

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1495	ASN	CG-OD1	23.53	1.75	1.24
3	C	1520	ASP	CG-OD2	11.48	1.51	1.25
3	C	1495	ASN	CB-CG	10.92	1.76	1.51
3	C	1602	LYS	CE-NZ	8.22	1.69	1.49
3	C	1518	GLY	C-O	7.93	1.36	1.23

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	504	ILE	C-N-CD	-21.38	73.56	120.60
1	A	504	ILE	C-N-CA	13.21	177.47	122.00
3	C	1495	ASN	CB-CG-ND2	7.48	134.66	116.70
3	C	1520	ASP	CB-CG-OD2	-7.36	111.68	118.30
1	A	574	VAL	CB-CA-C	-6.86	98.38	111.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	D	3000	NAG	C1

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	1635	VAL	Mainchain
1	D	290	GLN	Peptide
1	D	40	PHE	Peptide
1	D	504	ILE	Peptide
1	D	505	PRO	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4912	0	4976	88	0
1	D	4919	0	4986	112	0
2	B	1484	0	1511	22	0
2	E	1500	0	1526	22	0
3	C	2372	0	2280	30	0
3	F	2395	0	2302	23	0
4	G	113	0	98	0	0
4	H	113	0	98	6	0
5	A	28	0	25	1	0
5	D	28	0	25	1	0
6	A	1	0	0	0	0
6	C	1	0	0	0	0
6	D	2	0	0	0	0
6	F	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	8	0	0	3	0
7	B	3	0	0	0	0
7	C	1	0	0	0	0
7	D	15	0	0	5	0
7	E	3	0	0	0	0
7	F	2	0	0	0	0
8	A	30	0	40	7	0
8	B	6	0	8	1	0
8	C	6	0	8	1	0
8	D	42	0	56	16	0
8	E	12	0	16	5	0
8	F	6	0	8	5	0
8	H	6	0	8	0	0
9	A	111	0	0	1	0
9	B	47	0	0	1	0
9	C	23	0	0	0	0
9	D	188	0	0	4	0
9	E	62	0	0	1	0
9	F	35	0	0	1	0
9	H	5	0	0	0	0
All	All	18480	0	17971	285	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 285 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:1602:LYS:NZ	3:C:1602:LYS:CE	1.69	1.53
3:C:1495:ASN:CG	3:C:1495:ASN:CB	1.76	1.49
3:C:1495:ASN:CG	3:C:1495:ASN:OD1	1.75	1.24
1:D:139:ARG:HD2	8:D:807:GOL:H31	1.47	0.95
1:D:574:VAL:HG13	2:E:751:TRP:HE3	1.33	0.93

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	623/643 (97%)	583 (94%)	32 (5%)	8 (1%)	15	21
1	D	626/643 (97%)	587 (94%)	24 (4%)	15 (2%)	7	7
2	B	182/188 (97%)	172 (94%)	10 (6%)	0	100	100
2	E	184/188 (98%)	175 (95%)	7 (4%)	2 (1%)	17	25
3	C	286/343 (83%)	262 (92%)	16 (6%)	8 (3%)	6	5
3	F	289/343 (84%)	266 (92%)	17 (6%)	6 (2%)	9	10
4	G	13/15 (87%)	10 (77%)	2 (15%)	1 (8%)	1	0
4	H	13/15 (87%)	10 (77%)	2 (15%)	1 (8%)	1	0
All	All	2216/2378 (93%)	2065 (93%)	110 (5%)	41 (2%)	10	12

5 of 41 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	505	PRO
3	C	1593	LYS
1	D	41	PRO
1	D	78	LYS
1	D	290	GLN

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	555/567 (98%)	504 (91%)	51 (9%)	11	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	557/567 (98%)	512 (92%)	45 (8%)	15	22
2	B	171/175 (98%)	155 (91%)	16 (9%)	11	16
2	E	173/175 (99%)	159 (92%)	14 (8%)	15	22
3	C	266/309 (86%)	252 (95%)	14 (5%)	28	44
3	F	269/309 (87%)	256 (95%)	13 (5%)	31	49
4	G	11/11 (100%)	11 (100%)	0	100	100
4	H	11/11 (100%)	9 (82%)	2 (18%)	2	2
All	All	2013/2124 (95%)	1858 (92%)	155 (8%)	16	24

5 of 155 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	1420	ASN
1	D	140	THR
3	F	1401	ASN
3	C	1433	GLU
3	C	1532	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	1555	GLN
1	D	318	GLN
3	F	1620	ASN
1	D	155	GLN
1	D	332	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

4 carbohydrates are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	NAG	A	3000	1,5	14,14,15	0.53	0	15,19,21	0.89	0
5	NAG	A	3001	5	14,14,15	0.60	0	15,19,21	1.49	1 (6%)
5	NAG	D	3000	1,5	14,14,15	0.57	0	15,19,21	0.83	0
5	NAG	D	3001	5	14,14,15	0.66	0	15,19,21	1.50	2 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	3000	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	3001	5	-	0/6/23/26	0/1/1/1
5	NAG	D	3000	1,5	1/1/5/7	0/6/23/26	0/1/1/1
5	NAG	D	3001	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	3001	NAG	C3-C4-C5	3.39	116.11	110.20
5	D	3001	NAG	C4-C3-C2	3.94	117.36	111.23
5	A	3001	NAG	C1-O5-C5	5.05	118.66	112.25

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	D	3000	NAG	C1

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	3000	NAG	1	0
5	D	3000	NAG	1	0

5.6 Ligand geometry

Of 55 ligands modelled in this entry, 37 are monoatomic - leaving 18 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
8	GOL	A	802	-	5,5,5	0.48	0	5,5,5	0.71	0
8	GOL	A	809	-	5,5,5	0.54	0	5,5,5	0.36	0
8	GOL	A	816	-	5,5,5	0.42	0	5,5,5	0.57	0
8	GOL	A	821	-	5,5,5	0.34	0	5,5,5	0.28	0
8	GOL	A	845	-	5,5,5	0.43	0	5,5,5	0.27	0
8	GOL	B	915	-	5,5,5	0.35	0	5,5,5	0.55	0
8	GOL	C	819	-	5,5,5	0.34	0	5,5,5	0.16	0
8	GOL	D	807	-	5,5,5	0.45	0	5,5,5	0.36	0
8	GOL	D	811	-	5,5,5	0.28	0	5,5,5	0.35	0
8	GOL	D	818	-	5,5,5	0.37	0	5,5,5	0.29	0
8	GOL	D	822	-	5,5,5	0.29	0	5,5,5	0.69	0
8	GOL	D	823	-	5,5,5	0.40	0	5,5,5	0.29	0
8	GOL	D	824	-	5,5,5	0.35	0	5,5,5	0.37	0
8	GOL	D	825	-	5,5,5	0.39	0	5,5,5	0.32	0
8	GOL	E	915	-	5,5,5	0.29	0	5,5,5	0.18	0
8	GOL	E	916	-	5,5,5	0.29	0	5,5,5	0.56	0
8	GOL	F	840	-	5,5,5	0.42	0	5,5,5	0.42	0
8	GOL	H	820	-	5,5,5	0.26	0	5,5,5	0.40	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	GOL	A	802	-	-	0/4/4/4	0/0/0/0
8	GOL	A	809	-	-	0/4/4/4	0/0/0/0
8	GOL	A	816	-	-	0/4/4/4	0/0/0/0
8	GOL	A	821	-	-	0/4/4/4	0/0/0/0
8	GOL	A	845	-	-	0/4/4/4	0/0/0/0
8	GOL	B	915	-	-	0/4/4/4	0/0/0/0
8	GOL	C	819	-	-	0/4/4/4	0/0/0/0
8	GOL	D	807	-	-	0/4/4/4	0/0/0/0
8	GOL	D	811	-	-	0/4/4/4	0/0/0/0
8	GOL	D	818	-	-	0/4/4/4	0/0/0/0
8	GOL	D	822	-	-	0/4/4/4	0/0/0/0
8	GOL	D	823	-	-	0/4/4/4	0/0/0/0
8	GOL	D	824	-	-	0/4/4/4	0/0/0/0
8	GOL	D	825	-	-	0/4/4/4	0/0/0/0
8	GOL	E	915	-	-	0/4/4/4	0/0/0/0
8	GOL	E	916	-	-	0/4/4/4	0/0/0/0
8	GOL	F	840	-	-	0/4/4/4	0/0/0/0
8	GOL	H	820	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	802	GOL	1	0
8	A	809	GOL	6	0
8	B	915	GOL	1	0
8	C	819	GOL	1	0
8	D	807	GOL	3	0
8	D	811	GOL	3	0
8	D	818	GOL	2	0
8	D	822	GOL	2	0
8	D	823	GOL	2	0
8	D	824	GOL	2	0
8	D	825	GOL	2	0
8	E	916	GOL	5	0
8	F	840	GOL	5	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	631/643 (98%)	0.38	41 (6%) 22 22	31, 44, 58, 64	0
1	D	632/643 (98%)	0.33	4 (0%) 90 90	34, 44, 57, 67	0
2	B	184/188 (97%)	0.43	3 (1%) 74 74	38, 45, 56, 69	0
2	E	186/188 (98%)	0.38	3 (1%) 74 74	38, 45, 51, 63	0
3	C	292/343 (85%)	0.68	31 (10%) 8 8	38, 48, 59, 62	0
3	F	295/343 (86%)	0.50	25 (8%) 13 13	33, 46, 54, 59	0
4	G	13/15 (86%)	0.48	0 100 100	46, 50, 54, 55	0
4	H	13/15 (86%)	-0.33	0 100 100	35, 43, 50, 54	0
All	All	2246/2378 (94%)	0.42	107 (4%) 34 35	31, 45, 58, 69	0

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	914	ILE	7.0
2	B	914	ILE	6.7
2	B	913	GLY	5.6
3	C	1640	PRO	5.5
1	A	47	LEU	5.5

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	NAG	A	3000	14/15	0.82	0.14	-0.65	63,64,66,67	0
5	NAG	D	3000	14/15	0.90	0.15	-1.40	52,56,59,62	0
5	NAG	A	3001	14/15	0.83	0.35	-	68,69,69,69	0
5	NAG	D	3001	14/15	0.79	0.25	-	65,67,67,68	0

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
8	GOL	H	820	6/6	0.71	0.41	10.14	67,68,68,69	0
8	GOL	D	823	6/6	0.68	0.44	7.40	70,72,73,73	0
8	GOL	D	822	6/6	0.82	0.27	5.48	59,59,60,60	0
6	K	D	3003	1/1	0.83	0.26	4.74	80,80,80,80	0
8	GOL	A	821	6/6	0.69	0.21	2.68	86,86,87,87	0
8	GOL	A	802	6/6	0.59	0.24	2.37	52,53,53,54	0
8	GOL	A	816	6/6	0.84	0.27	2.24	46,50,50,52	0
8	GOL	A	809	6/6	0.79	0.29	1.50	67,67,67,67	0
8	GOL	B	915	6/6	0.91	0.22	1.27	52,52,52,53	0
8	GOL	E	916	6/6	0.84	0.23	1.06	43,44,45,45	0
7	BR	D	719	1/1	0.99	0.16	0.83	40,40,40,40	1
8	GOL	C	819	6/6	0.83	0.23	0.74	68,68,68,69	0
8	GOL	D	824	6/6	0.77	0.20	0.46	62,62,63,63	0
8	GOL	D	811	6/6	0.86	0.17	0.38	35,43,44,46	0
8	GOL	D	807	6/6	0.94	0.17	0.08	41,43,46,46	0
8	GOL	A	845	6/6	0.85	0.14	0.05	58,60,60,60	0
7	BR	D	720	1/1	0.97	0.18	-0.05	45,45,45,45	1
8	GOL	F	840	6/6	0.82	0.16	-0.19	53,54,54,55	0
8	GOL	D	825	6/6	0.79	0.18	-0.56	50,53,56,56	0
6	K	A	3002	1/1	0.99	0.11	-0.97	57,57,57,57	0
7	BR	A	730	1/1	0.84	0.15	-1.19	50,50,50,50	1
8	GOL	E	915	6/6	0.85	0.14	-1.61	57,58,58,58	0
7	BR	D	710	1/1	0.97	0.12	-2.22	52,52,52,52	1
6	K	F	605	1/1	0.96	0.08	-2.27	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	BR	A	724	1/1	0.93	0.12	-2.30	61,61,61,61	1
6	K	C	602	1/1	0.97	0.10	-2.33	64,64,64,64	0
7	BR	A	715	1/1	0.89	0.09	-2.56	52,52,52,52	1
7	BR	F	701	1/1	0.97	0.09	-2.73	59,59,59,59	1
7	BR	E	702	1/1	0.99	0.07	-2.79	60,60,60,60	0
7	BR	D	705	1/1	0.97	0.10	-3.24	54,54,54,54	1
7	BR	D	703	1/1	0.98	0.08	-4.52	54,54,54,54	1
6	K	D	3002	1/1	0.96	0.08	-5.61	41,41,41,41	0
7	BR	B	706	1/1	0.98	0.06	-5.82	42,42,42,42	1
7	BR	D	727	1/1	0.69	0.15	-	45,45,45,45	1
7	BR	D	713	1/1	0.94	0.12	-	53,53,53,53	1
7	BR	A	712	1/1	0.98	0.16	-	39,39,39,39	1
7	BR	E	707	1/1	0.95	0.09	-	62,62,62,62	1
7	BR	A	711	1/1	0.95	0.05	-	96,96,96,96	0
7	BR	D	718	1/1	0.98	0.19	-	53,53,53,53	1
7	BR	D	729	1/1	0.94	0.08	-	63,63,63,63	1
7	BR	E	709	1/1	0.94	0.11	-	59,59,59,59	1
7	BR	D	716	1/1	0.97	0.14	-	45,45,45,45	1
7	BR	B	722	1/1	0.93	0.12	-	54,54,54,54	1
7	BR	D	732	1/1	0.96	0.14	-	33,33,33,33	1
7	BR	A	723	1/1	0.93	0.10	-	40,40,40,40	1
7	BR	C	731	1/1	0.90	0.28	-	50,50,50,50	1
7	BR	D	725	1/1	0.95	0.10	-	52,52,52,52	1
7	BR	D	728	1/1	0.89	0.10	-	49,49,49,49	1
8	GOL	D	818	6/6	0.75	0.25	-	48,52,55,56	0
7	BR	F	726	1/1	0.96	0.09	-	58,58,58,58	1
7	BR	D	714	1/1	0.95	0.10	-	62,62,62,62	1
7	BR	A	708	1/1	0.97	0.13	-	44,44,44,44	1
7	BR	A	717	1/1	0.96	0.12	-	57,57,57,57	1
7	BR	D	704	1/1	0.97	0.11	-	43,43,43,43	1
7	BR	B	721	1/1	0.95	0.12	-	59,59,59,59	1

6.5 Other polymers

There are no such residues in this entry.